SANOFI

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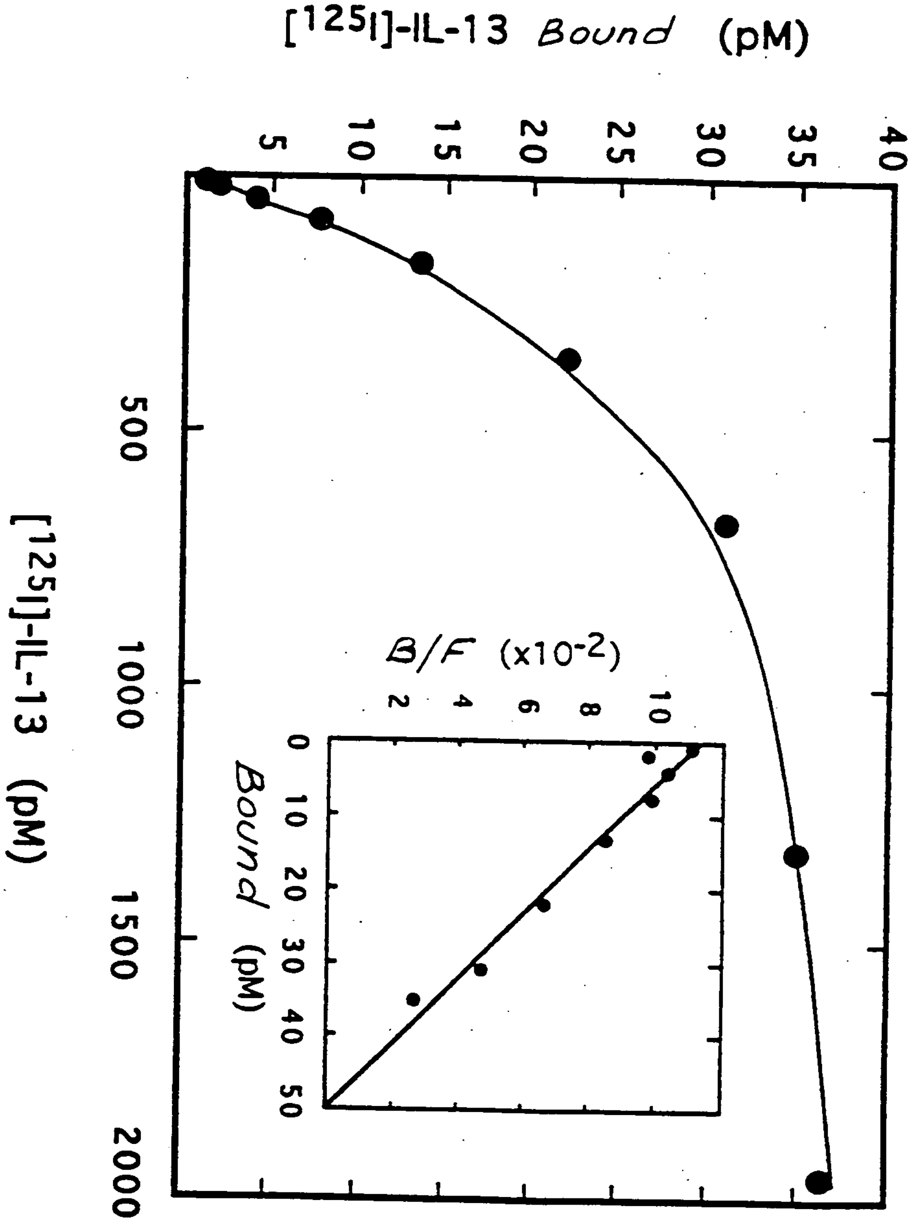

FIG.1a

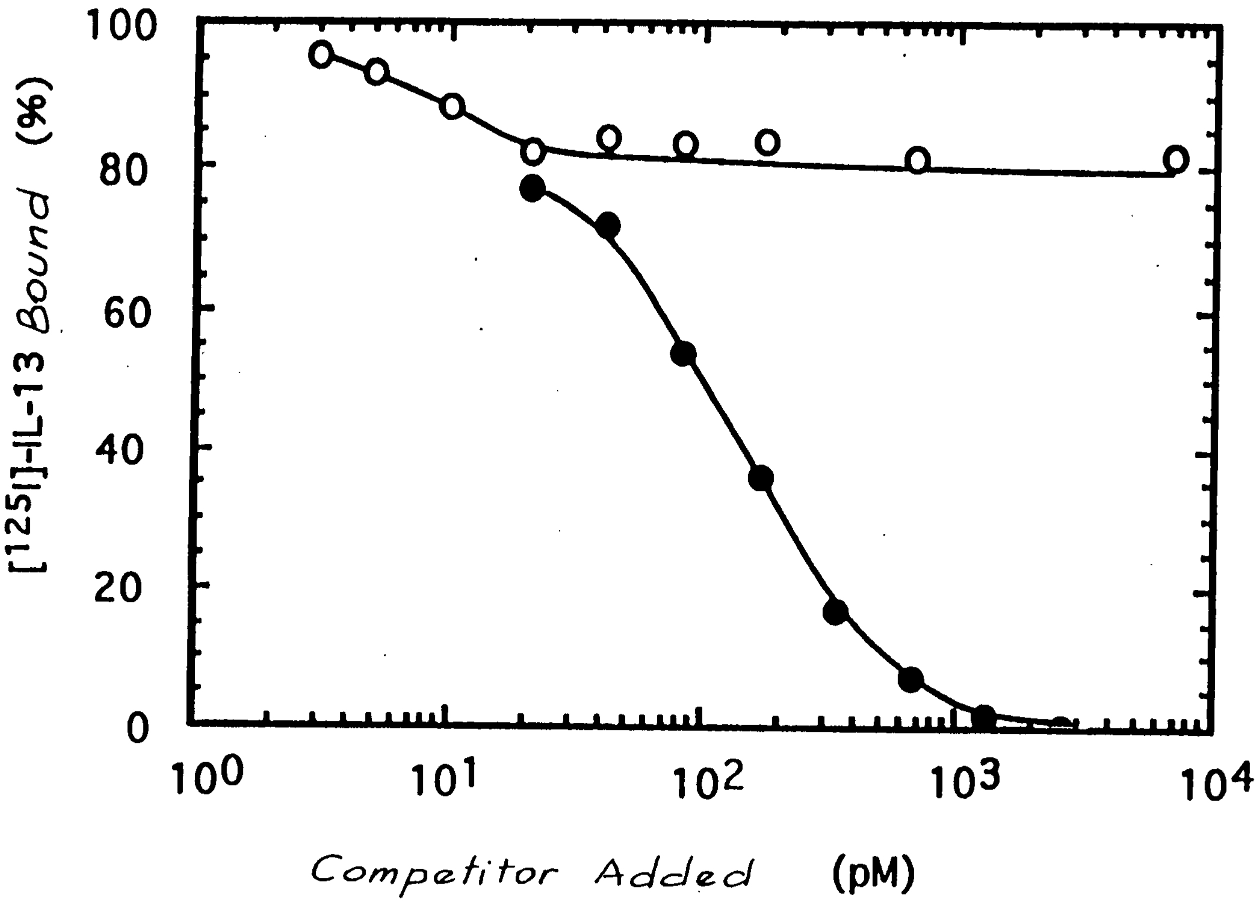
100
80
60
40
20
0
[125I]-IL-13 Bound (%)
10^0
10^1
10^2
10^3
10^4
Competitor Added (pM)

FIG.1b

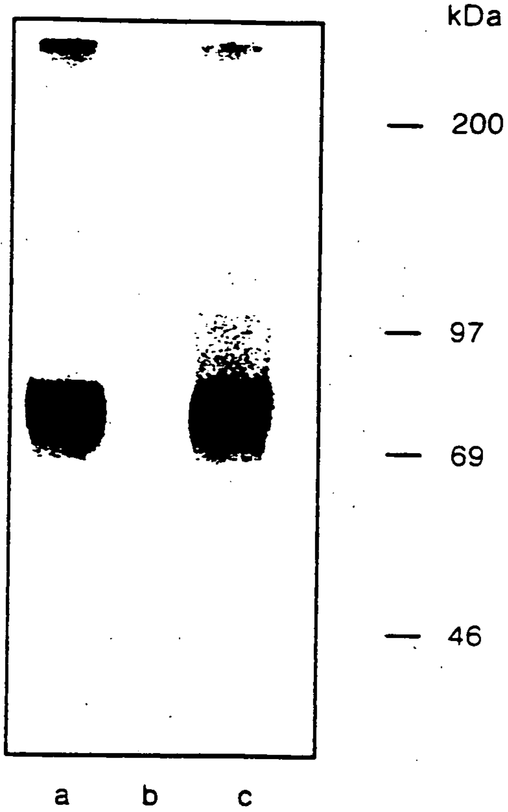

FIG. 1c

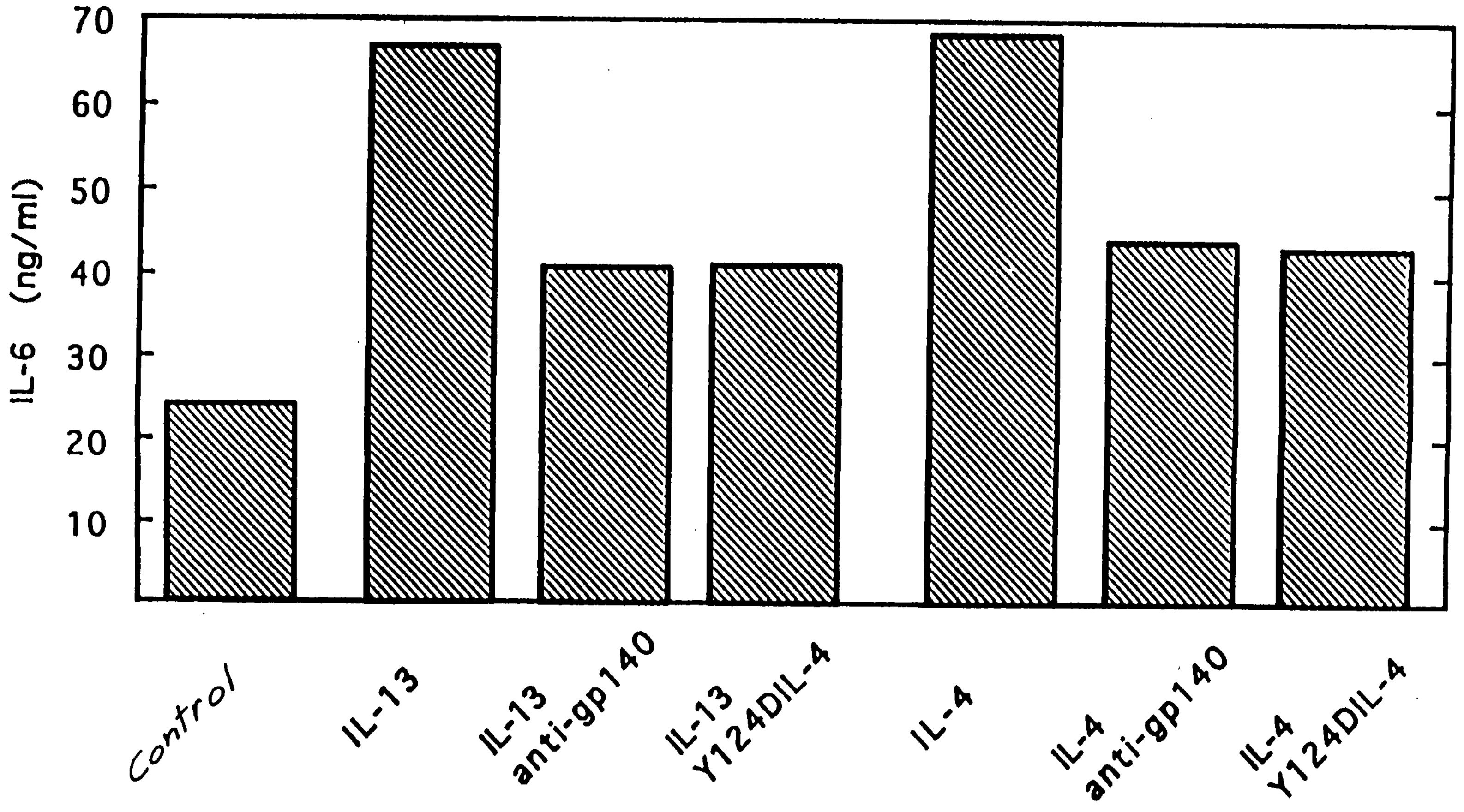
IL-6 (ng/ml)
70
60
50
40
30
20
10
Control
IL-13
IL-13 anti-gp140
IL-13 Y124DIL-4
IL-4
IL-4 anti-gp140
IL-4 Y124DIL-4

FIG.1d

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```
  1   GGTGCCTGTCGGCGGGGAGAGAGGCAATATCAAGGTTTTAAATCTCGGAGAAATGGCT   58
  1                                                       MetAla    2

 59  TTCGTTTGCTTGGCTATCGGATGCTTATATACCTTTCTGATAAGCACAACATTTGGCTGT  118
  3  PheValCysLeuAlaIleGlyCysLeuTyrThrPheLeuIleSerThrThrPheGlyCys   22

119  ACTTCATCTTCAGACACCGAGATAAAAGTTAACCCTCCTCAGGATTTTGAGATAGTGGAT  178
 23  ThrSerSerSerAspThrGluIleLysValAsnProProGlnAspPheGluIleValAsp   42

179  CCCGGATACTTAGGTTATCTCTATTTGCAATGGCAACCCCCACTGTCTCTGGATCATTTT  238
 43  ProGlyTyrLeuGlyTyrLeuTyrLeuGlnTrpGlnProProLeuSerLeuAspHisPhe   62

239  AAGGAATGCACAGTGGAATATGAACTAAAATACCGAAACATTGGTAGTGAAACATGGAAG  298
 63  LysGluCysThrValGluTyrGluLeuLysTyrArgAsnIleGlySerGluThrTrpLys   82

299  ACCATCATTACTAAGAATCTACATTACAAAGATGGGTTTGATCTTAACAAGGGCATTGAA  358
 83  ThrIleIleThrLysAsnLeuHisTyrLysAspGlyPheAspLeuAsnLysGlyIleGlu  102

359  GCGAAGATACACACGCTTTTACCATGGCAATGCACAAATGGATCAGAAGTTCAAAGTTCC  418
103  AlaLysIleHisThrLeuLeuProTrpGlnCysThrAsnGlySerGluValGlnSerSer  122

419  TGGGCAGAAACTACTTATTGGATATCACCACAAGGAATTCCAGAAACTAAAGTTCAGGAT  478
123  TrpAlaGluThrThrTyrTrpIleSerProGlnGlyIleProGluThrLysValGlnAsp  142

479  ATGGATTGCGTATATTACAATTGGCAATATTTACTCTGTTCTTGGAAACCTGGCATAGGT  538
143  MetAspCysValTyrTyrAsnTrpGlnTyrLeuLeuCysSerTrpLysProGlyIleGly  162

539  GTACTTCTTGATACCAATTACAACTTGTTTTACTGGTATGAGGGCTTGGATCATGCATTA  598
163  ValLeuLeuAspThrAsnTyrAsnLeuPheTyrTrpTyrGluGlyLeuAspHisAlaLeu  182

599  CAGTGTGTTGATTACATCAAGGCTGATGGACAAAATATAGGATGCAGATTTCCCTATTTG  658
183  GlnCysValAspTyrIleLysAlaAspGlyGlnAsnIleGlyCysArgPheProTyrLeu  202
```

FIG.2a

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```
659   GAGGCATCAGACTATAAAGATTTCTATATTTGTGTTAATGGATCATCAGAGAACAAGCCT   718
203   GluAlaSerAspTyrLysAspPheTyrIleCysValAsnGlySerSerGluAsnLysPro   222

719   ATCAGATCCAGTTATTTCACTTTTCAGCTTCAAAATATAGTTAAACCTTTGCCGCCAGTC   778
223   IleArgSerSerTyrPheThrPheGlnLeuGlnAsnIleValLysProLeuProProVal   242

779   TATCTTACTTTTACTCGGGAGAGTTCATGTGAAATTAAGCTGAAATGGAGCATACCTTTG   838
243   TyrLeuThrPheThrArgGluSerSerCysGluIleLysLeuLysTrpSerIleProLeu   262

839   GGACCTATTCCAGCAAGGTGTTTTGATTATGAAATTGAGATCAGAGAAGATGATACTACC   898
263   GlyProIleProAlaArgCysPheAspTyrGluIleGluIleArgGluAspAspThrThr   282

899   TTGGTGACTGCTACAGTTGAAAATGAAACATACACCTTGAAAACAACAAATGAAACCCGA   958
283   LeuValThrAlaThrValGluAsnGluThrTyrThrLeuLysThrThrAsnGluThrArg   302

959   CAATTATGCTTTGTAGTAAGAAGCAAAGTGAATATTTATTGCTCAGATGACGGAATTTGG   1018
303   GlnLeuCysPheValValArgSerLysValAsnIleTyrCysSerAspAspGlyIleTrp   322

1019  AGTGAGTGGAGTGATAAACAATGCTGGGAAGGTGAAGACCTATCGAAGAAAACTTTGCTA   1078
323   SerGluTrpSerAspLysGlnCysTrpGluGlyGluAspLeuSerLysLysThrLeuLeu   342

1079  CGTTTCTGGCTACCATTTGGTTTCATCTTAATATTAGTTATATTTGTAACCGGTCTGCTT   1138
343   ArgPheTrpLeuProPheGlyPheIleLeuIleLeuValIlePheValThrGlyLeuLeu   362

1139  TTGCGTAAGCCAAACACCTACCCAAAAATGATTCCAGAATTTTTCTGTGATACATGAAGA   1198
363   LeuArgLysProAsnThrTyrProLysMetIleProGluPhePheCysAspThr         381

1199  CTTTCCATATCAAGAGACATGGTATTGACTCAACAGTTTCCAGTCATGGCCAAATGTTCA   1258
1259  ATATGAGTCTCAATAAACTGAATTTTTCTTGCGAATGTTG   1298
```

FIG. 2a (continuation)

```
                    .         .         .         .         .
IL13R           MAFVCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLY 50
                      |   |               |  |   ||  | |   | |
IL5R            ..MIIVAHVLLILLGATEILQADLLPDEKISLLPPVNFTIKVTG.LAQVL 47

                    .         .         .         .         .
IL13R           LQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKG 100
                ||| |            ::  |          | ||     |    | ||
IL5R            LQWKPNPDQEQ.RNVNLEYQVKINAPKEDDYETRITES...KCVTILHKG 93

                    .         .         .         .         .
IL13R           IEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV.... 146
                  |   | |       |   ||||       | | | |      |
IL5R            FSASVRTILQ...NDHSLLASSWASAE.LHAPPGSPGTSIVNLTCTTNTT 139

                    .         .         .         .         .
IL13R           ..YYNWQ.....YLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIK 189
                   |         : | :  |     || | | | |        |  | |
IL5R            EDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE..ECQEYSK 187

                    .         .         .         .         .
IL13R           AD.GQNIGCRFP..YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIV 236
                   | || | |:               |||||    ||     | |  |
IL5R            DTLGRNIACWFPRTFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAID 237

                    .         .         .         .         .
IL13R           KPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTA 286
                   ||   |   :        |  |    |  |||||  |
IL5R            QINPPLNVTAEIEGT.RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQI 286

                    .         .         .         .         .
IL13R           TVENETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDL 336
                                     ||  |   |   | |||||      | |
IL5R            EKLMTNAFISIIDDLSKYDVQVRAAVSSMCREAGLWSEWSQ.PIYVGNDE 335

                    .         .         .         .         .
IL13R           SKKTLLRFWLPFGFILILVIFVTGLLLRKPNTYPKMIP..........EF 376
                 |     |                |         |  |
IL5R            HKPLREWFVIVIMATICFILLILSLICKICHLWIKLFPPIPAPKSNIKDL 385

                    .         .         .
IL13R           FCDT................................ 380
                |  |
IL5R            FVTTNYEKAGSSETEIEVICYIEKPGVETLEDSVF 420
```

FIG. 2b

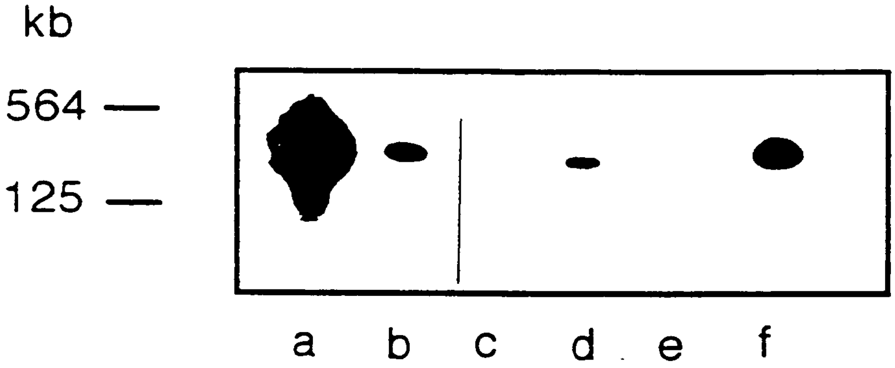


FIG.3

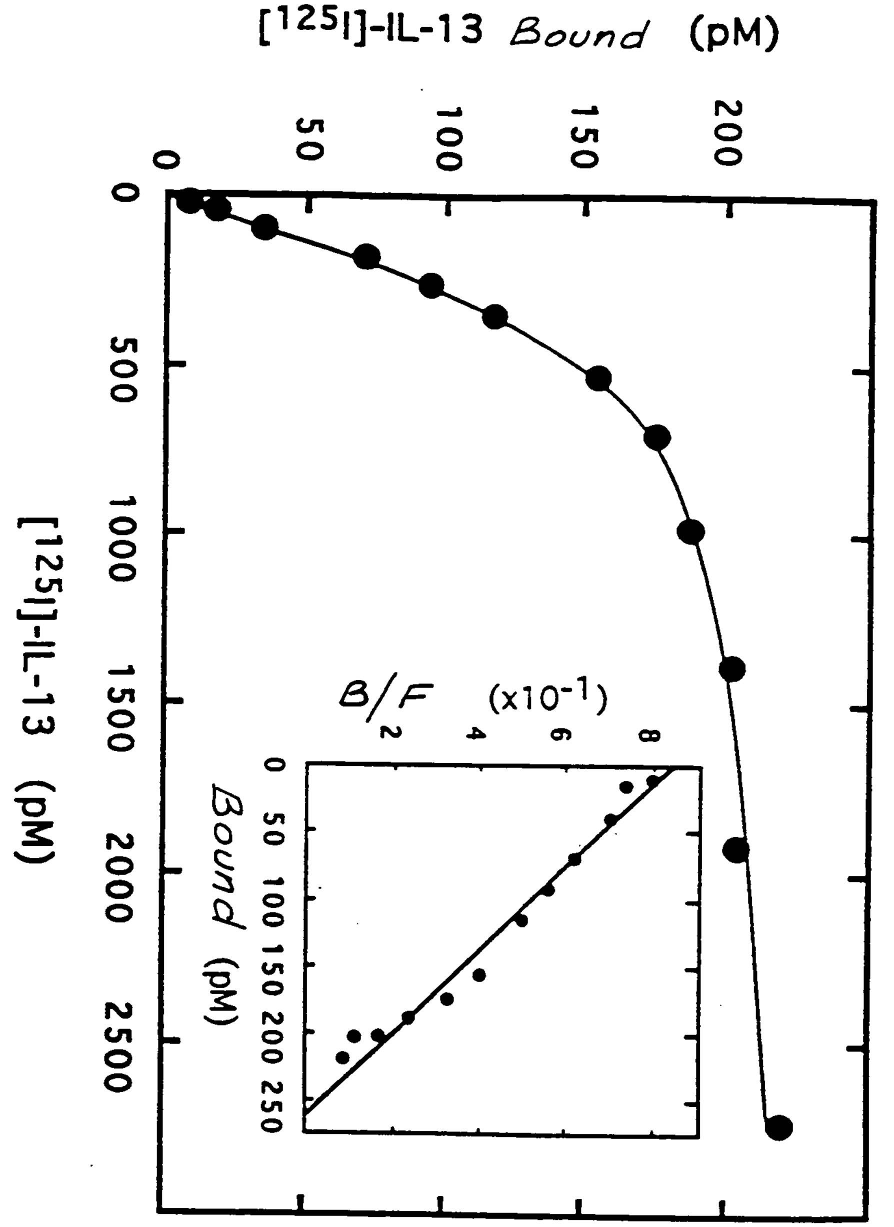

[125I]-IL-13 Bound (pM)
0
50
100
150
200
0
500
1000
1500
2000
2500
[125I]-IL-13 (pM)
B/F (x10-1)
2
4
6
8
0
50
100
150
200
250
Bound (pM)

FIG. 4a

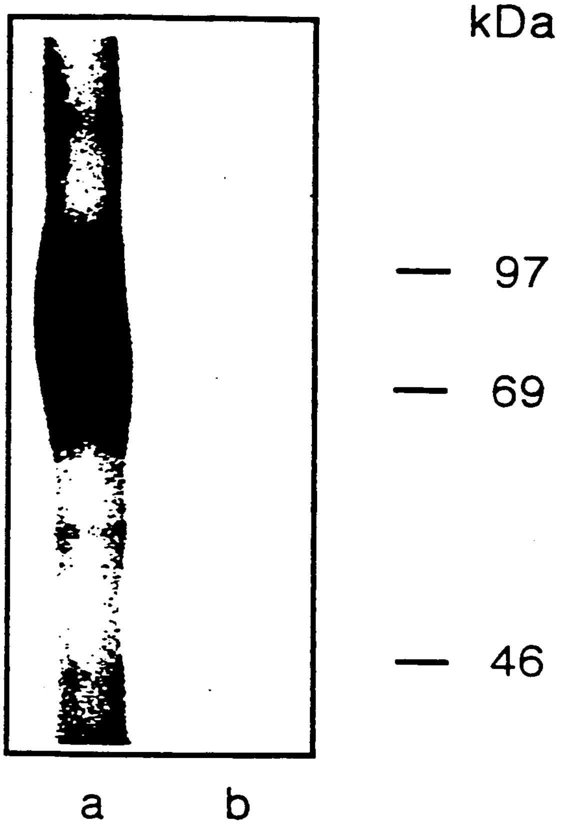


FIG.4b

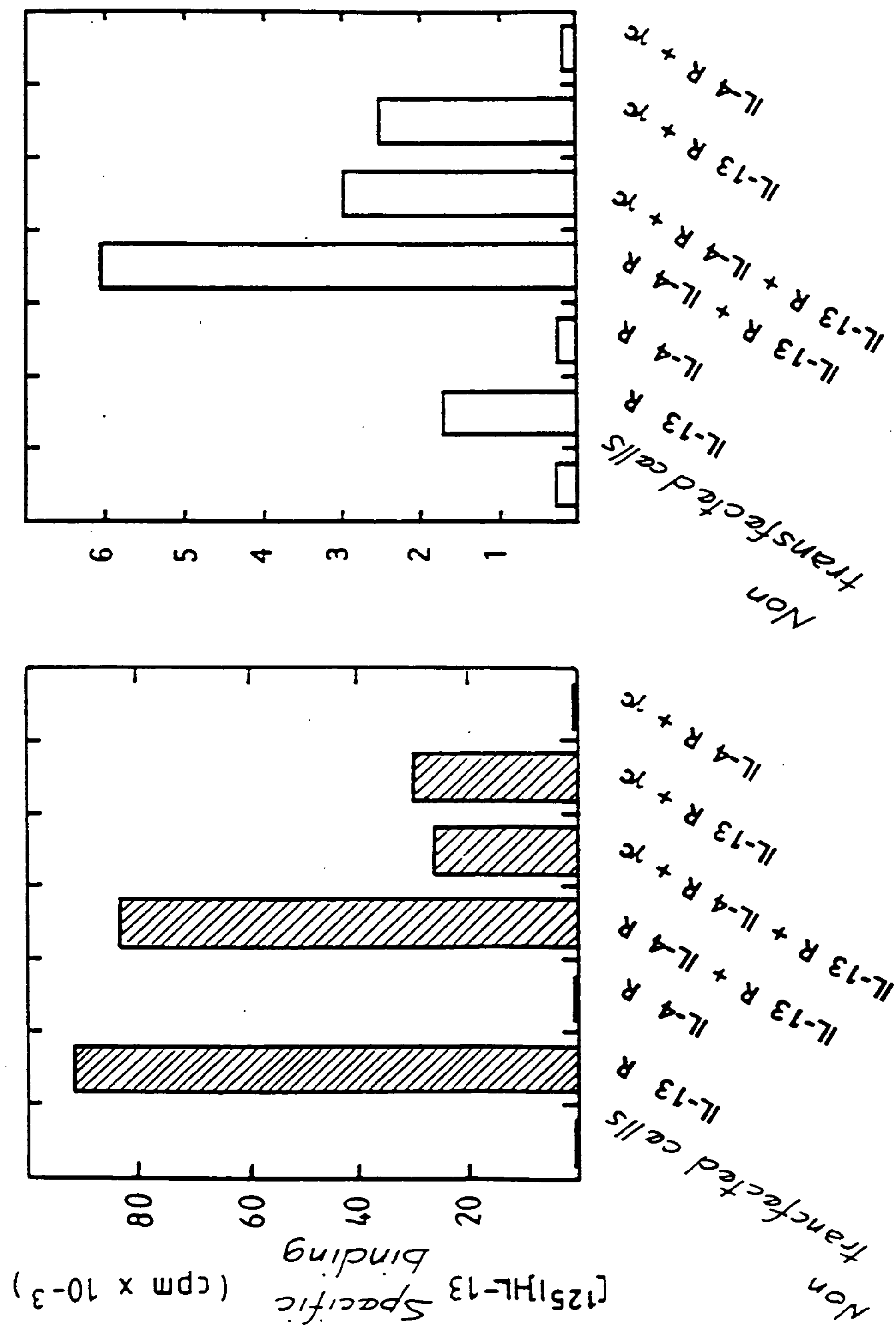

[125I]IL-13 Specific binding (cpm x 10-3)
80
60
40
20
6
5
4
3
2
1
Non tranfected cells
IL-13 R
IL-4 R
IL-13 R + IL-4 R
IL-13 R + IL-4 R + γc
IL-13 R + γc
IL-4 R + γc
Non transfected cells
IL-13 R
IL-4 R
IL-13 R + IL-4 R
IL-13 R + IL-4 R + γc
IL-13 R + γc
IL-4 R + γc

FIG.4C

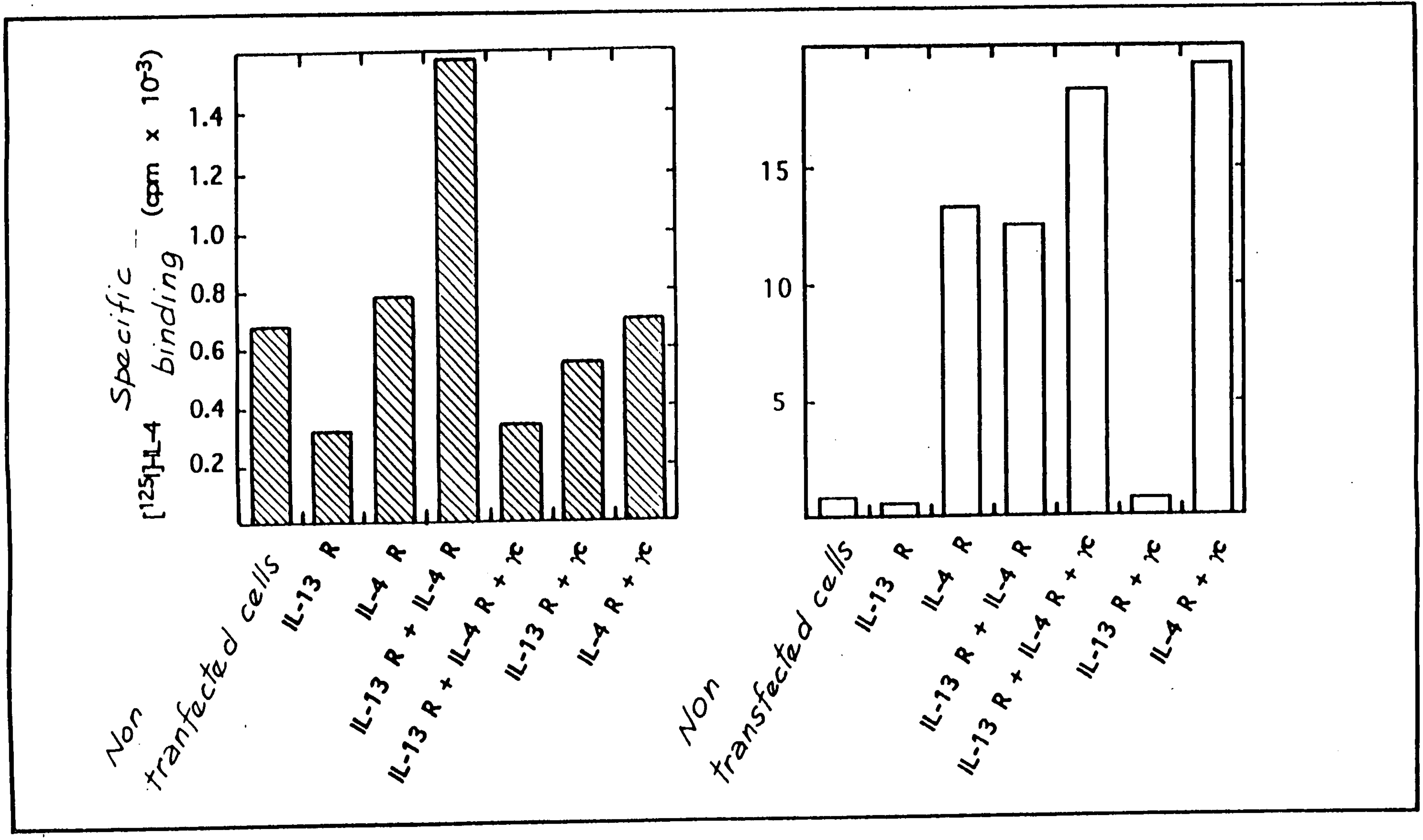

Specific [^{125}I]IL-4 binding (cpm x 10^{-3})
1.4
1.2
1.0
0.8
0.6
0.4
0.2
Non tranfected cells
IL-13 R
IL-4 R
IL-13 R + IL-4 R
IL-13 R + IL-4 R + γc
IL-13 R + γc
IL-4 R + γc
15
10
5
Non transfected cells
IL-13 R
IL-4 R
IL-13 R + IL-4 R
IL-13 R + IL-4 R + γc
IL-13 R + γc
IL-4 R + γc

FIG.4d

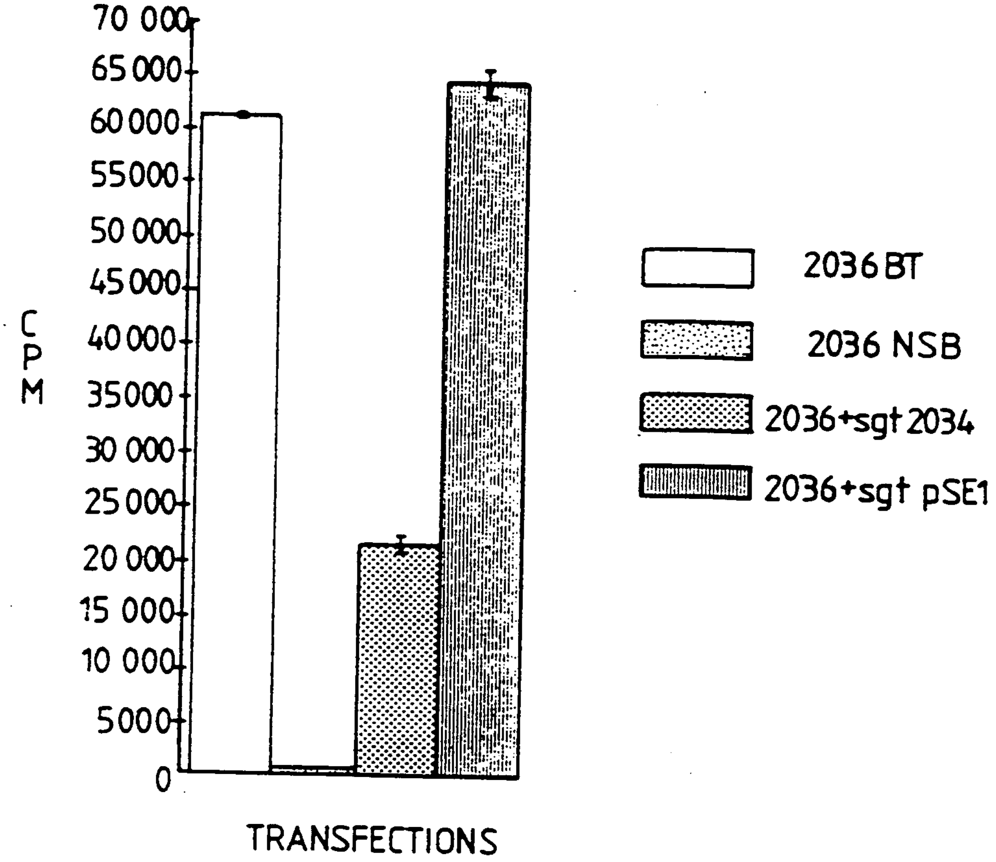
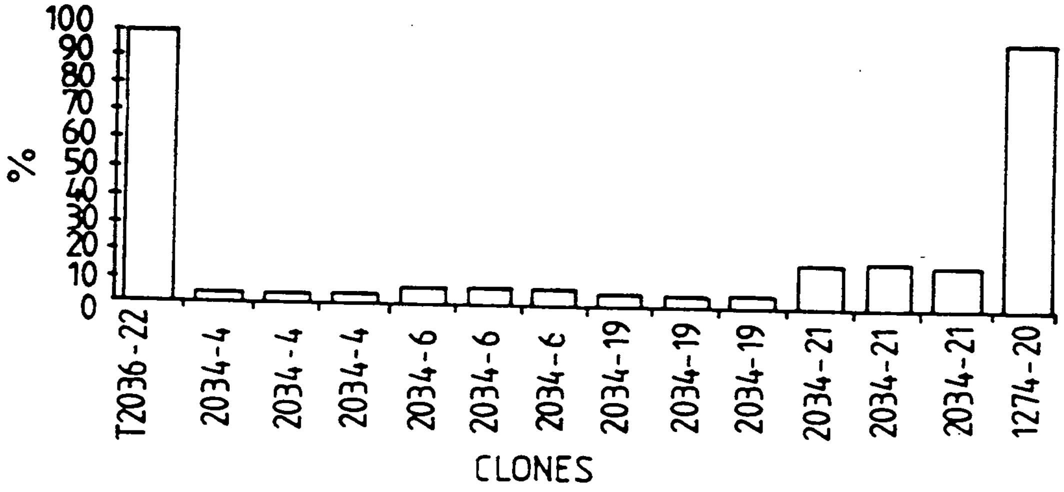

70 000
65 000
60 000
55000
50 000
45 000
40 000
35000
30 000
25 000
20 000
15 000
10 000
5000
0
CPM
TRANSFECTIONS
2036 BT
2036 NSB
2036+sgt 2034
2036+sgt pSE1

FIG. 5

FIG. 6


100
90
80
70
60
50
40
30
20
10
0
%
T2036-22
2034-4
2034-4
2034-4
2034-6
2034-6
2034-6
2034-19
2034-19
2034-19
2034-21
2034-21
2034-21
1274-20
CLONES

```
    1  TCAGCCCGGCCGGGCTCCGAGGCGAGAGGCTGCATGGAGTGGCCGGCGCGGCTCTGCGGG    60
  -10                                    M  E  W  P  A  R  L  C  G      9
   61  CTGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGCGGGGGCGGGGGCGCCGCGCCTACG   120
   10   L  W  A  L  L  L  C  A  G  G  G  G  G  G  G  G  A  A  P  T     29
  121  GAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATA   180
   30   E  T  Q  P  P  V  T  N  L  S  V  S  V  E  N  L  C  T  V  I     49
  181  TGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCAT   240
   50   W  T  W  N  P  P  E  G  A  S  S  N  C  S  L  W  Y  F  S  H     69
  241  TTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACCC   300
   70   F  G  D  K  Q  D  K  K  I  A  P  E  T  R  R  S  I  E  V  P     89
  301  CtGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAG   360
   90   L  N  E  R  I  C  L  Q  V  G  S  Q  C  S  T  N  E  S  E  K    109
  361  CCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTG   420
  110   P  S  I  L  V  E  K  C  I  S  P  P  E  G  D  P  E  S  A  V    129
  421  ACTGAGCTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTGGCTCCCTGGA   480
  130   T  E  L  Q  C  I  W  H  N  L  S  Y  M  K  C  S  W  L  P  G    149
  481  AGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAA   540
  150   R  N  T  S  P  D  T  N  Y  T  L  Y  Y  W  H  R  S  L  E  K    169
  541  ATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCCTTTGATCTG   600
  170   I  H  Q  C  E  N  I  F  R  E  G  Q  Y  F  G  C  S  F  D  L    189
  601  ACCAAAGTGAAGGATTCCAGTTTtGAACAACACAGTGTCCAAATAATGGTCAAGGATAAT   660
  190   T  K  V  K  D  S  S  F  E  Q  H  S  V  Q  I  M  V  K  D  N    209
  661  GCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGAT   720
  210   A  G  K  I  K  P  S  F  N  I  V  P  L  T  S  R  V  K  P  D    229
  721  CCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAAT   780
  230   P  P  H  I  K  N  L  S  F  H  N  D  D  L  Y  V  Q  W  E  N    249
  781  CCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACT   840
  250   P  Q  N  F  I  S  R  C  L  F  Y  E  V  E  V  N  N  S  Q  T    269
  841  GAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGA   900
  270   E  T  H  N  V  F  Y  V  Q  E  A  K  C  E  N  P  E  F  E  R    289
  901  AATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACA   960
  290   N  V  E  N  T  S  C  F  M  V  P  G  V  L  P  D  T  L  N  T    309
  961  GTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAAT  1020
  310   V  R  I  R  V  K  T  N  K  L  C  Y  E  D  D  K  L  W  S  N    329
 1021  TGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTA  1080
  330   W  S  Q  E  M  S  I  G  K  K  R  N  S  T  L  Y  I  T  M  L    349
 1081  CTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAGG  1140
  350   L  I  V  P  V  I  V  A  G  A  I  I  V  L  L  L  Y  L  K  R    369
 1141  CTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTTT  1200
  370   L  K  I  I  I  F  P  P  I  P  D  P  G  K  I  F  K  E  M  F    389
 1201  GGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACC  1260
  390   G  D  Q  N  D  D  T  L  H  W  K  K  Y  D  I  Y  E  K  Q  T    409
 1261  AAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGG  1320
  410   K  E  E  T  D  S  V  V  L  I  E  N  L  K  K  A  S  Q  *       429
```

FIG.7a

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```
1381   TATCTGGGAACTTATTAAATGGAAACTGAAACTACTGCACCATTTAAAAACAGGCAGCTC   1440
1441   ATAAGAGCCACAGGTCTTTATGTTGAGTCGCGCACCGAAAAACTAAAAATAATGGGCGCT   1500
1501   TTGGAGAAGAGTGTGGAGTCATTCTCATTGAATTATAAAAGCCAGCAGGCTTCAAACTAG   1560
1561   GGGACAAAGCAAAAAGTGATGATAGTGGTGGAGTTAATCTTATCAAGAGTTGTGACAACT   1620
1621   TCCTGAGGGATCTATACTTGCTTTGTGTTCTTTGTGTCAACATGAACAAATTTTATTTGT   1680
1681   AGGGGAACTCATTTGGGGTGCAAATGCTAATGTCAAACTTGAGTCACAAAGAACATGTAG   1740
1741   AAAACAAAATGGATAAAATCTGATATGTATTGTTTGGGATCCTATTGAACCATGTTTGTG   1800
1801   GCTATTAAAACTCTTTTAACAGTCTGGGCTGGGTCCGGTGGCTCACGCCTGTAATCCCAG   1860
1861   CAATTTGGGAGTCCGAGGCGGGCGGATCACTCGAGGTCAGGAGTTCCAGACCAGCCTGAC   1920
1921   CAAAATGGTGAAACCTCCTCTCTACTAAAACTACAAAAATTAACTGGGTGTGGTGGCGCG   1980
1981   TGCCTGTAATCCCAGCTACTCGGGAAGCTGAGGCAGGTGAATTGTTTGAACCTGGGAGGT   2040
2041   GGAGGTTGCAGTGAGCAGAGATCACACCACTGCACTCTAGCCTGGGTGACAGAGCAAGAC   2100
2101   TCTGTCTAAAAAACAAAACAAAACAAAACAAAACAAAAAAACCTCTTAATATTCTGGAGT   2160
2161   CATCATTCCCTTCGACAGCATTTTCCTCTGCTTTGAAAGCCCCAGAAATCAGTGTTGGCC   2220
2221   ATGATGACAACTACAGAAAAACCAGAGGCAGCTTCTTTGCCAAGACCTTTCAAAGCCATT   2280
2281   TTAGGCTGTTAGGGGCAGTGGAGGTAgAATGACTCCTTGGGTATTAGAGTTTCAACCATG   2340
2341   AAGTCTCTAACAATGTaTTTTCTTCACCTCTGCTACTCAAGTAGCATTTACTGTGTCTTT   2400
2401   GGTTTGTGCTAGGCCCCCGGGTGTGAAGCACAGACCCCTTCCAGGGGTTTACAGTCTATt   2460
2461   TGAGACTCCTCAGTTCTTGCCACTTTTTTTTTAATCTCCACCAGTCATTTTTCAGACCT   2520
2521   TTTAACTCCTCAATTCCAACACTGATTTCCCCTTTTGCATTCTCCCTCCTTCCCTTCCTT   2580
2581   GTAGCCTTTTGACTTTCATTGGAAATTAGGATGTAAATCTGCTCAGGAGACCTGGAGGAG   2640
2641   CAGAGGATAATTAGCATCTCAGGTTAAGTGTGAGTAATCTGAGAAACAATGACTAATTCT   2700
2701   TGCATATTTTGTAACTTCCATGTGAGGGTTTTCAGCATTGATATTTGTGCATTTTCTAAA   2760
2761   CAGAGATGAGGTGGTATCTTCACGTAGAACATTGGTATTCGCTTGAGAAAAAAAGAATAG   2820
2821   TTGAACCTATTTCTCTTTCTTTACAAGATGGGTCCAGGATTCCTCTTTTCTCTGCCATAA   2880
2881   ATGATTAATTAAATAGCTTTTGTGTCTTACATTGGTAGCCAGCCAGCCAAGGCTCTGTTT   2940
2941   ATGCTTTTGGGGGGCATATATTGGGTTCCATTCTCACCTATCCACACAACATATCCGTAT   3000
3001   ATATCCCCTCTACTCTTACTTCCCCCAAATTTAAAGAAGTATGGGAAATGAGAGGCATTT   3060
3061   CCCCCACCCCATTTCTCTCCTCACACACAGACTCATATTACTGGTAGGAACTTGAGAACT   3120
3121   TTATTTCCAAGTTGTTCAAACATTTACCAATCATATTAATACAATGATGCTATTTGCAAT   3180
3181   TCCTGCTCCTAGGGGAGGGGAGATAAGAAACCCTCACTCTCTACAGGTTTGGGTACAAGT   3240
3241   GGCAACCTGCTTCCATGGCCGTGTAGAAGCATGGTGCCCTGGCTTCTCTGAGGAAGCTGG   3300
3301   GGTTCATGACAATGGCAGATGTAAAGTTATTCTTGAAGTCAGATTGAGGCTGGGAGACAG   3360
3361   CCGTAGTAGATGTTCTACTTTGTTCTGCTGTTCTCTAGAAAGAATATTTGGTTTTCCTGT   3420
3421   ATAGGAATGAGATTAATTCCTTTCCAGGTATTTTATAATTCTGGGAAGCAAAACCCATGC   3480
3481   CTCCCCCTAGCCATTTTTACTGTTATCCTATTTAGATGGCCATGAAGAGGATGCTGTGAA   3540
3541   ATTCCCAACAAACATTGATGCTGACAGTCATGCAGTCTGGGAGTGGGGAAGTGATCTTTT   3600
3601   GTTCCCATCCTCTTCTTTTAGCAGTAAAATAGCTGAGGGAAAAGGGAGGGAAAAGGAAGT   3660
3661   TATGGGAATACCTGTGGTGGTTGTGATCCCTAGGTCTTGGGAGCTCTTGGAGGTGTCTGT   3720
3721   ATCAGTGGATTTCCCATCCCCTGTGGGAAATTAGTAGGCTCATTTACTGTTTTAGGTCTA   3780
3781   GCCTATGTGGATTTTTTCCTAACATACCTAAGCAAACCCAGTGTCAGGATGGTAATTCTT   3840
3841   ATTCTTTCGTTCAGTTAAGTTTTTCCCTTCATCTGGGCACTGAAGGGATATGTGAAACAA   3900
3901   TGTTAACATTTTTGGTAGTCTTCAACCAGGGATTGTTTCTGTTTAACTTCTTATAGGAAA   3960
3961   GCTTGAGTAAAATAAATATTGTCTTTTTGTATGTCACCCaaaaaaaaaa   4009
```

FIG. 7a (continuation)

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IL-13α HUMAN

IL-13α MOUSE

```
   1 MEWPARLCGLWALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIW  50
     |.:|| |.:|:.|||   .:..|..||:||.||||||||||||||||:||
   1 MARPALLGELLVLLL..WTATVGQVAAATEVQPPVTNLSVSVENLCTIIW  48

  51 TWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGS 100
     ||.||||||.||.|:|||||:|.|||||||||:|. |:||:|:|||||||
  49 TWSPPEGASPNCTLRYFSHFDDQQDKKIAPETHRKEELPLDEKICLQVGS  98

 101 QCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGR 150
     |||.||||||| ||.|||||||||||||||||.|||||||||||||||||
  99 QCSANESEKPSPLVKKCISPPEGDPESAVTELKCIWHNLSYMKCSWLPGR 148

 151 NTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQH 200
     ||||||:||||||..|||| :|||||:||||.::|||.|||| :.|||::
 149 NTSPDTHYTLYYWYSSLEKSRQCENIYREGQHIACSFKLTKV.EPSFEHQ 197

 201 SVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENP 250
     .||||||||||||:|| .||.||| |||||||||:| :.|:.|.|||.||
 198 NVQIMVKDNAGKIRPSCKIVSLTSYVKPDPPHIKHLLLKNGALLVQWKNP 247

 251 QNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP 300
     ||| |||| |||||||.||: ||:: |:|.||:|.| :||:|.|||| :|
 248 QNFRSRCLTYEVEVNNTQTDRHNILEVEEDKCQNSESDRNMEGTSCFQLP 297

 301 GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLL 350
     |||:|.: |||:||||||||::|:||||:||:. ||||..|||:|.||||
 298 GVLADAVYTVRVRVKTNKLCFDDNKLWSDWSEAQSIGKEQNSTFYTTMLL 347

 351 IVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWK 400
     .:||:||.|:|:||:|||||||||||||||||||||||||||||||||||
 348 TIPVFVAVAVIILLFYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWK 397

 401 KYDIYEKQTKEETDSVVLIENLKKASQ 427
     ||||||||.||||||||||||||||..
 398 KYDIYEKQSKEETDSVVLIENLKKAAP 424
```

FIG. 7b

09077817 .051498

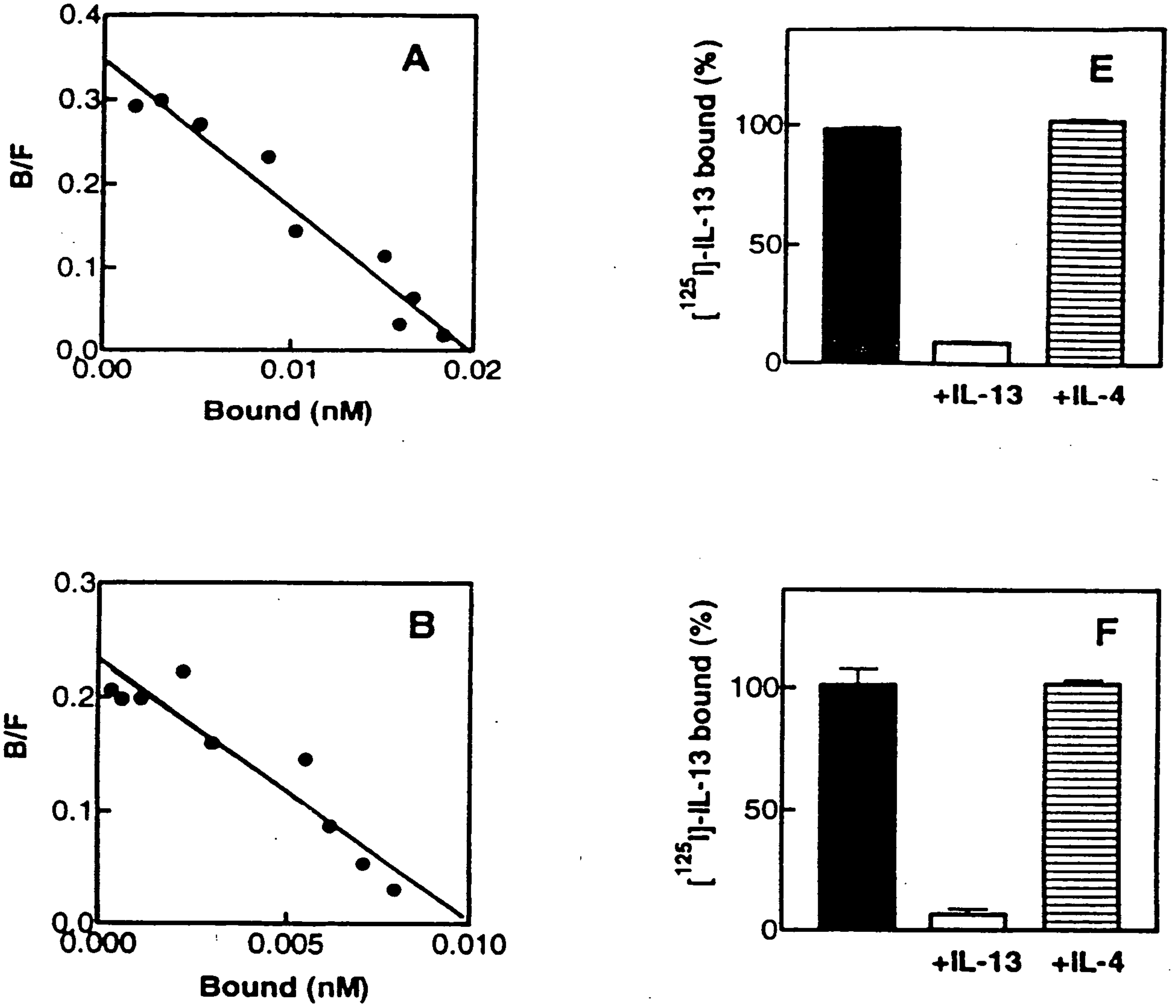
A
B/F
0.4
0.3
0.2
0.1
0.0
0.00
0.01
0.02
Bound (nM)
E
[^{125}I]-IL-13 bound (%)
100
50
0
+IL-13
+IL-4
B
B/F
0.3
0.2
0.1
0.0
0.000
0.005
0.010
Bound (nM)
F
[^{125}I]-IL-13 bound (%)
100
50
0
+IL-13
+IL-4

FIG.8

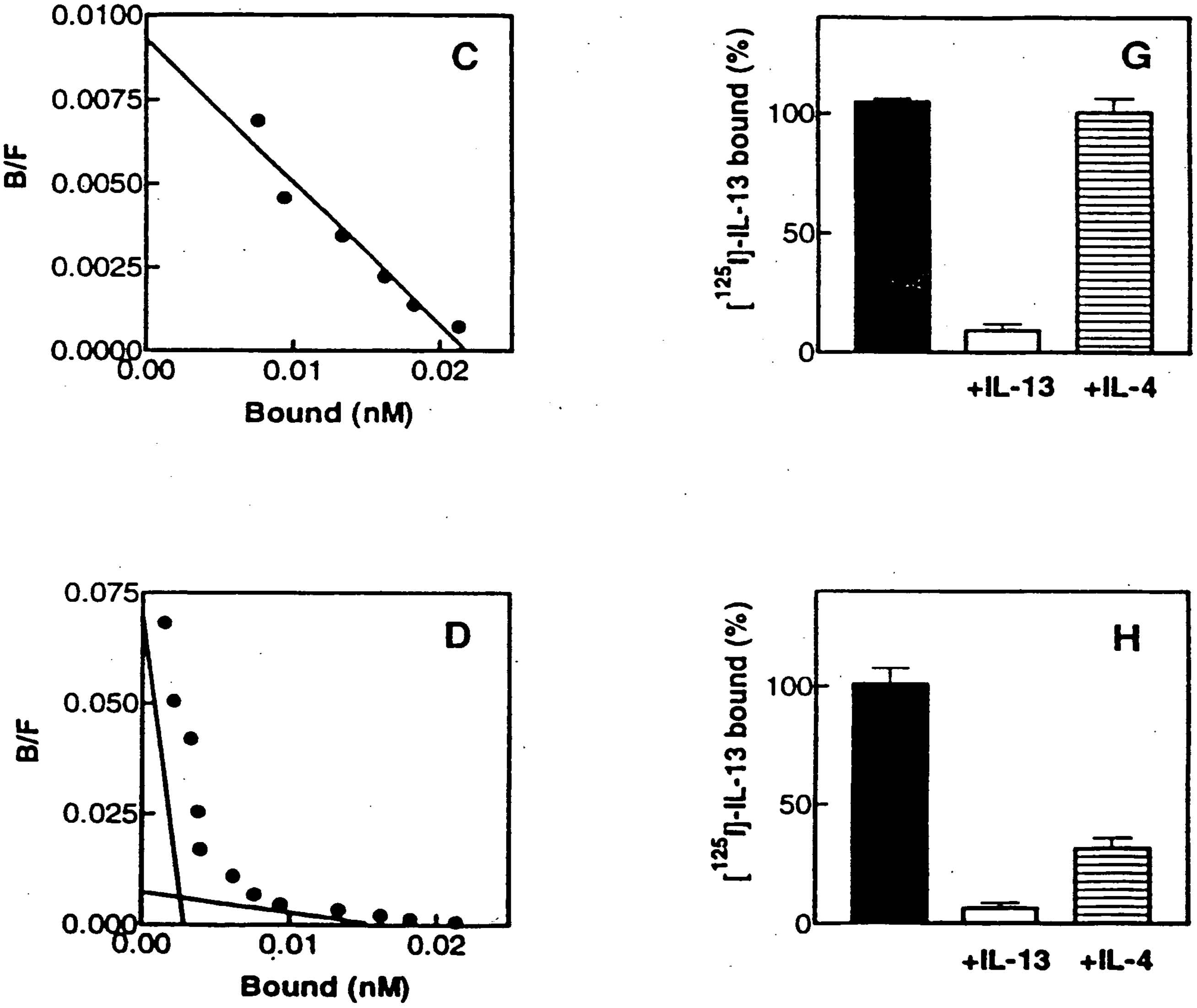

FIG. 8 (continuation)

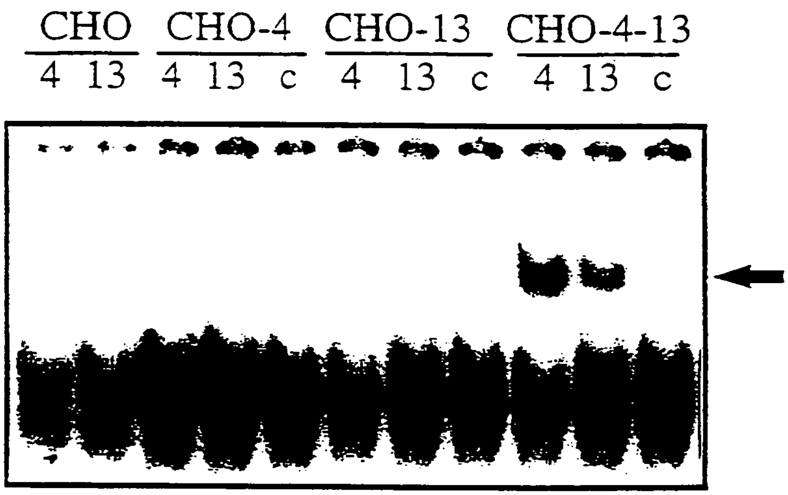

FIG.9